RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/552,014A
Source: IFW00
Date Processed by STIC: 05/08/2006

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IFWO

RAW SEQUENCE LISTING DATE: 05/08/2006
PATENT APPLICATION: **US/10/552,014A** TIME: 10:53:45

Input Set : **A:\3172us0pSeqCORR.txt**
Output Set: **N:\CRF4\05082006\J552014A.raw**

<110> APPLICANT: ITO, Yasuaki
FUJII, Ryo
KOBAYASHI, Makoto
HINUMA, Shuji
HASHIMOTO, Tadatoshi
TANAKA, Yasuhiro
<120> TITLE OF INVENTION: Novel Screening Method
<130> FILE REFERENCE: 3172US0P
<140> CURRENT APPLICATION NUMBER: 10/552,014A
<141> CURRENT FILING DATE: 2005-10-12
<150> PRIOR APPLICATION NUMBER: PCT/JP2004/005947
<151> PRIOR FILING DATE: 2004-04-23
<150> PRIOR APPLICATION NUMBER: JP 2003-122464
<151> PRIOR FILING DATE: 2003-04-25
<160> NUMBER OF SEQ ID NOS: 15
<210> SEQ ID NO: 1
<211> LENGTH: 453
<212> TYPE: PRT
<213> ORGANISM: Human
<400> SEQUENCE: 1

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His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr
            20                  25                  30
Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn
        35                  40                  45
Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
    50                  55                  60
Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
65                  70                  75                  80
Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
                85                  90                  95
Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr
            100                 105                 110
Phe Leu Phe Glu Ala Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
        115                 120                 125
Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys
    130                 135                 140
Ala Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp
145                 150                 155                 160
Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr
                165                 170                 175
Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn
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```
54              180                 185                 190
55 Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser
56          195                 200                 205
57 Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile
58      210                 215                 220
59 Phe Gly Ala Phe Val Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe
60 225                 230                 235                 240
61 Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser
62                  245                 250                 255
63 Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu
64              260                 265                 270
65 Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile
66          275                 280                 285
67 Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile
68      290                 295                 300
69 Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg
70 305                 310                 315                 320
71 Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser
72                  325                 330                 335
73 Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg
74              340                 345                 350
75 Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala
76          355                 360                 365
77 Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser
78      370                 375                 380
79 Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser
80 385                 390                 395                 400
81 Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu
82                  405                 410                 415
83 Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu
84              420                 425                 430
85 Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe
86          435                 440                 445
87 Gln Glu His Glu Val
88      450
90 <210> SEQ ID NO: 2
91 <211> LENGTH: 1359
92 <212> TYPE: DNA
93 <213> ORGANISM: Human
95 <400> SEQUENCE: 2
96 atggcttcac ccagcctccc gggcagtgac tgctcccaaa tcattgatca cagtcatgtc    60
97 cccgagtttg aggtggccac ctggatcaaa atcaccctta ttctggtgta cctgatcatc   120
98 ttcgtgatgg gccttctggg gaacagcgcc accattcggg tcacccaggt gctgcagaag   180
99 aaaggatact tgcagaagga ggtgacagac cacatggtga gtttggcttg ctcggacatc   240
100 ttggtgttcc tcatcggcat gcccatggag ttctacagca tcatctggaa tcccctgacc   300
101 acgtccagct acaccctgtc ctgcaagctg cacactttcc tcttcgaggc ctgcagctac   360
102 gctacgctgc tgcacgtgct gacactcagc tttgagcgct acatcgccat ctgtcacccc   420
103 ttcaggtaca aggctgtgtc gggaccttgc caggtgaagc tgctgattgg cttcgtctgg   480
104 gtcacctccg ccctggtggc actgcccttg ctgtttgcca tgggtactga gtaccccctg   540
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105 gtgaacgtgc ccagccaccg gggtctcact tgcaaccgct ccagcacccg ccaccacgag 600
106 cagcccgaga cctccaatat gtccatctgt accaacctct ccagccgctg gaccgtgttc 660
107 cagtccagca tcttcggcgc cttcgtggtc tacctcgtgg tcctgctctc cgtagccttc 720
108 atgtgctgga acatgatgca ggtgctcatg aaaagccaga agggctcgct ggccgggggc 780
109 acgcggcctc cgcagctgag gaagtccgag agcgaagaga gcaggaccgc caggaggcag 840
110 accatcatct tcctgaggct gattgttgtg acattggccg tatgctggat gcccaaccag 900
111 attcggagga tcatggctgc ggccaaaccc aagcacgact ggacgaggtc ctacttccgg 960
112 gcgtacatga tcctcctccc cttctcggag acgtttttct acctcagctc ggtcatcaac 1020
113 ccgctcctgt acacggtgtc ctcgcagcag tttcggcggg tgttcgtgca ggtgctgtgc 1080
114 tgccgcctgt cgctgcagca cgccaaccac gagaagcgcc tgcgcgtaca tgcgcactcc 1140
115 accaccgaca gcgcccgctt tgtgcagcgc ccgttgctct tcgcgtcccg gcgccagtcc 1200
116 tctgcaagga gaactgagaa gattttctta agcactttc agagcgaggc cgagccccag 1260
117 tctaagtccc agtcattgag tctcgagtca ctagagccca actcaggcgc gaaaccagcc 1320
118 aattctgctg cagagaatgg ttttcaggag catgaagtt 1359
120 <210> SEQ ID NO: 3
121 <211> LENGTH: 20
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: primer
128 <400> SEQUENCE: 3
129 tgtgacattg gccgtatgct 20
131 <210> SEQ ID NO: 4
132 <211> LENGTH: 19
133 <212> TYPE: DNA
134 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:
137 <223> OTHER INFORMATION: primer
139 <400> SEQUENCE: 4
140 cagtcgtgct tgggtttgg 19
142 <210> SEQ ID NO: 5
143 <211> LENGTH: 24
144 <212> TYPE: DNA
145 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
148 <223> OTHER INFORMATION: primer
150 <400> SEQUENCE: 5
151 tgcccaacca gattcggagg atca 24
153 <210> SEQ ID NO: 6
155 <211> LENGTH: 456
156 <212> TYPE: PRT
157 <213> ORGANISM: Mouse
159 <400> SEQUENCE: 6
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161 5 10 15
162 His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr
163 20 25 30
164 Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Val Gly Ile Leu Gly Asn
165 35 40 45

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166 Ser Val Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
167      50                  55                  60
168 Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
169  65                  70                  75                  80
170 Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
171                  85                  90                  95
172 Asn Pro Leu Thr Thr Pro Ser Tyr Ala Leu Ser Cys Lys Leu His Thr
173             100                 105                 110
174 Phe Leu Phe Glu Thr Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
175         115                 120                 125
176 Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Lys Tyr Lys
177     130                 135                 140
178 Ala Val Ser Gly Pro Arg Gln Val Lys Leu Leu Ile Gly Phe Val Trp
179 145                 150                 155                 160
180 Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Ile
181                 165                 170                 175
182 Glu Tyr Pro Leu Val Asn Val Pro Thr His Lys Gly Leu Asn Cys Asn
183             180                 185                 190
184 Leu Ser Arg Thr Arg His His Asp Glu Pro Gly Asn Ser Asn Met Ser
185         195                 200                 205
186 Ile Cys Thr Asn Leu Ser Asn Arg Trp Glu Val Phe Gln Ser Ser Ile
187     210                 215                 220
188 Phe Gly Ala Phe Ala Val Tyr Leu Val Val Leu Ala Ser Val Ala Phe
189 225                 230                 235                 240
190 Met Cys Trp Asn Met Met Lys Val Leu Met Lys Ser Lys Gln Gly Thr
191                 245                 250                 255
192 Leu Ala Gly Thr Gly Pro Gln Leu Gln Leu Arg Lys Ser Glu Ser Glu
193             260                 265                 270
194 Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile
195         275                 280                 285
196 Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile
197     290                 295                 300
198 Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Thr Tyr Phe Arg
199 305                 310                 315                 320
200 Ala Tyr Met Ile Leu Leu Pro Phe Ser Asp Thr Phe Phe Tyr Leu Ser
201                 325                 330                 335
202 Ser Val Val Asn Pro Leu Leu Tyr Asn Val Ser Ser Gln Gln Phe Arg
203             340                 345                 350
204 Lys Val Phe Trp Gln Val Leu Cys Cys Arg Leu Thr Leu Gln His Ala
205         355                 360                 365
206 Asn Gln Glu Lys Arg Gln Arg Ala Arg Phe Ile Ser Thr Lys Asp Ser
207     370                 375                 380
208 Thr Ser Ser Ala Arg Ser Pro Leu Ile Phe Leu Ala Ser Arg Arg Ser
209 385                 390                 395                 400
210 Asn Ser Ser Ser Arg Arg Thr Asn Lys Val Phe Leu Ser Thr Phe Gln
211                 405                 410                 415
212 Thr Glu Ala Lys Pro Gly Glu Ala Lys Pro Gln Pro Leu Ser Pro Glu
213             420                 425                 430
214 Ser Pro Gln Thr Gly Ser Glu Thr Lys Pro Ala Gly Ser Thr Pro Glu
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Input Set : **A:\3172us0pSeqCORR.txt**
Output Set: **N:\CRF4\05082006\J552014A.raw**

215 435 440 445
216 Asn Ser Leu Gln Glu Gln Glu Val
217 450 455
219 <210> SEQ ID NO: 7
221 <211> LENGTH: 1368
222 <212> TYPE: DNA
223 <213> ORGANISM: Mouse
225 <400> SEQUENCE: 7
226 atggcttcat ccagtggctc caaccacatc tgctcccgtg tcatcgatca tagccatgtt 60
227 cctgaatttg aggtggccac ttggatcaaa atcaccctca tcttggtgta cctgatcatt 120
228 tttgtggtag gcatcttggg caacagcgtc accatcaggg ttacgcaggt attgcagaag 180
229 aagggctatt tgcagaagga ggtgacagat cacatggtca gtttggcttg ttcagatatc 240
230 ttggtctttt tgattggcat gcccatggag ttctacagca tcatttggaa ccccctgacc 300
231 acacccagct atgctctgtc ctgtaagctc cacacgttcc tctttgagac gtgcagctac 360
232 gccacactgc tgcacgtgct gaccctcagc tttgagcgct acattgccat ttgtcatccc 420
233 ttcaagtata aagcagtgtc tggacctcgc caggtgaaac tgctgattgg ctttgtatgg 480
234 gtcacctccg ccctggtggc actgcctttg ctctttgcca tgggtatcga gtaccctctg 540
235 gtaaacgtac ccactcacaa gggactcaac tgcaacctct ctcgcacccg ccaccacgat 600
236 gaacctggaa actccaatat gtccatctgc acgaacctct ccaaccgttg ggaggtcttc 660
237 cagtccagca tctttggggc ctttgctgtt tacctggtgg tcctggcgtc tgtggctttc 720
238 atgtgttgga atatgatgaa agtgctaatg aagagcaagc agggcactct tgcagggacc 780
239 gggccacagc tccagctgag gaagtcagag agtgaggaga gccggacagc aagaagacag 840
240 accatcatat tcctgagact gattgtggtg acgttggccg tgtgttggat gcccaatcag 900
241 atccgacgga tcatggctgc agcaaaaccc aaacatgact ggaccagaac gtacttcagg 960
242 gcatacatga tcctcctgcc cttctctgat accttcttct acctcagctc tgtggtcaac 1020
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244 tgccgcctga ctctgcagca tgccaaccaa gagaaacgcc agcgtgcccg cttcatctcc 1140
245 accaaggaca gcaccagctc agcccgcagc cccctcatct tcctagcctc ccggcgcagt 1200
246 aactcttcct ccaggagaac taacaaggtt ttcttaagca cttttcagac tgaggccaag 1260
247 cctggagagg ctaagcccca gcccttgagt cctgagtcac cacagactgg ctcagagacc 1320
248 aaaccagctg ggtccacccc agaaaatagt ttacaggagc aggaagta 1368
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252 <211> LENGTH: 456
253 <212> TYPE: PRT
254 <213> ORGANISM: Rat
256 <400> SEQUENCE: 8
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258 5 10 15
259 His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr
260 20 25 30
261 Leu Thr Leu Val Tyr Leu Ile Val Phe Val Val Gly Ile Leu Gly Asn
262 35 40 45
263 Ser Val Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
264 50 55 60
265 Gln Lys Glu Val Thr Asp His Met Ile Ser Leu Ala Cys Ser Asp Ile
266 65 70 75 80
267 Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
268 85 90 95
269 Asn Pro Leu Thr Thr Pro Ser Tyr Ala Leu Ser Cys Lys Leu His Thr

VERIFICATION SUMMARY DATE: 05/08/2006
PATENT APPLICATION: **US/10/552,014A** TIME: 10:53:46

Input Set : **A:\3172us0pSeqCORR.txt**
Output Set: **N:\CRF4\05082006\J552014A.raw**